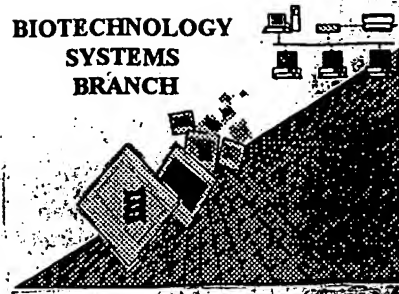


0280

BIOTECHNOLOGY
SYSTEMS
BRANCH



**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/026,952
Source: OPE
Date Processed by STIC: 1/14/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/026 952

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000 *correct format*
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 26 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/026,952

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

5 <110> APPLICANT: Nazarenko, Irina
 7 Rashtchian, Ayoub
 9 Solus, Joseph
 11 Pires, Richard M.
 13 Darfler, Marlene
 15 Gebeyehu, Gulilat
 17 Astatke, Mekbib
 21 <120> TITLE OF INVENTION: Primers and Methods for the Detection and Discrimination of
 Nucleic
 22 Acids
 26 <130> FILE REFERENCE: 0942.4980006
 30 <140> CURRENT APPLICATION NUMBER: US/10/026,952
 30 <141> CURRENT FILING DATE: 2001-12-27
 30 <150> PRIOR APPLICATION NUMBER: 60/330,468
 32 <151> PRIOR FILING DATE: 2001-10-23
 36 <150> PRIOR APPLICATION NUMBER: 60/139,890
 38 <151> PRIOR FILING DATE: 1999-06-22
 42 <150> PRIOR APPLICATION NUMBER: 60/175,959
 44 <151> PRIOR FILING DATE: 2000-01-13
 48 <150> PRIOR APPLICATION NUMBER: 09/599,594
 50 <151> PRIOR FILING DATE: 2000-06-22
 54 <150> PRIOR APPLICATION NUMBER: 09/748,146
 56 <151> PRIOR FILING DATE: 2000-12-27
 60 <160> NUMBER OF SEQ ID NOS: 139
 64 <170> SOFTWARE: PatentIn version 3.1
 68 <210> SEQ ID NO: 1
 70 <211> LENGTH: 23
 72 <212> TYPE: DNA
 74 <213> ORGANISM: Artificial Sequence
 78 <220> FEATURE:
 80 <223> OTHER INFORMATION: Primer
 82 <220> FEATURE:
 84 <221> NAME/KEY: misc_feature
 86 <222> LOCATION: (18)..(18)
 88 <223> OTHER INFORMATION: Fluorescently labeled
 92 <400> SEQUENCE: 1
 93 ccttctcatg gtggctgtag aac
 96 <210> SEQ ID NO: 2
 98 <211> LENGTH: 23
 100 <212> TYPE: DNA
 102 <213> ORGANISM: Artificial Sequence
 106 <220> FEATURE:
 108 <223> OTHER INFORMATION: Primer
 110 <220> FEATURE:
 112 <221> NAME/KEY: misc_feature
 114 <222> LOCATION: (1)..(1)
 116 <223> OTHER INFORMATION: Fluorescently labeled
 120 <400> SEQUENCE: 2

PP. 3, 4, 6

23

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

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121 ccttctcatg gtggctgtag aac 23
124 <210> SEQ ID NO: 3
126 <211> LENGTH: 23
128 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
136 <223> OTHER INFORMATION: Primer
138 <400> SEQUENCE: 3 23
139 ggtctacagc caccatgaga agg
142 <210> SEQ ID NO: 4
144 <211> LENGTH: 23
146 <212> TYPE: DNA
148 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
154 <223> OTHER INFORMATION: Primer
156 <400> SEQUENCE: 4 23
157 ggggctgcga ctgtgctccg gca
160 <210> SEQ ID NO: 5
162 <211> LENGTH: 23
164 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
172 <223> OTHER INFORMATION: Primer
174 <400> SEQUENCE: 5 23
175 tgccggagca cagtcgcagc ccc
178 <210> SEQ ID NO: 6
180 <211> LENGTH: 20
182 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
190 <223> OTHER INFORMATION: Primer
192 <220> FEATURE:
194 <221> NAME/KEY: misc_feature
196 <222> LOCATION: (1)..(1)
198 <223> OTHER INFORMATION: Fluorescently labeled
202 <400> SEQUENCE: 6 20
203 aataatagga tgaggcagga
206 <210> SEQ ID NO: 7
208 <211> LENGTH: 20
210 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
218 <223> OTHER INFORMATION: Primer
220 <220> FEATURE:
222 <221> NAME/KEY: misc_feature
224 <222> LOCATION: (1)..(1)
226 <223> OTHER INFORMATION: Labeled with BODIPY 530/550
230 <400> SEQUENCE: 7 20
231 aataatagga tgaggcagga

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

234 <210> SEQ ID NO: 8
236 <211> LENGTH: 20
238 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
246 <223> OTHER INFORMATION: Primer
248 <400> SEQUENCE: 8
249 tcctgcctca tcctattatt 20
252 <210> SEQ ID NO: 9
254 <211> LENGTH: 23
256 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:
264 <223> OTHER INFORMATION: Primer
266 <400> SEQUENCE: 9 23
267 gagttgaccg taacagacat ctt
270 <210> SEQ ID NO: 10
272 <211> LENGTH: 24
274 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
282 <223> OTHER INFORMATION: Primer
284 <400> SEQUENCE: 10 24
285 ggcattgccg acaggatgta gaag
288 <210> SEQ ID NO: 11
290 <211> LENGTH: 18
292 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
300 <223> OTHER INFORMATION: Primer
302 <400> SEQUENCE: 11 18
303 gggccggact cgtcatac
306 <210> SEQ ID NO: 12
308 <211> LENGTH: 28
310 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
318 <223> OTHER INFORMATION: Primer
320 <400> SEQUENCE: 12 28
321 ggttgtagag cactcagcac aatgaaga
324 <210> SEQ ID NO: 13
326 <211> LENGTH: 23
328 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
336 <223> OTHER INFORMATION: Primer
338 <400> SEQUENCE: 13
W--> 339 000
342 <210> SEQ ID NO: 14

*incorrect format for
an intentionally skipped
sequence (see item 8 on
Error Summary
Sheet)*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

```

344 <211> LENGTH: 23
346 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
352 <220> FEATURE:
354 <223> OTHER INFORMATION: Primer
356 <400> SEQUENCE: 14
357 ccttctcatg gtggctgtag aac
360 <210> SEQ ID NO: 15
362 <211> LENGTH: 23
364 <212> TYPE: DNA
366 <213> ORGANISM: Artificial Sequence
370 <220> FEATURE:
372 <223> OTHER INFORMATION: Primer
374 <400> SEQUENCE: 15
375 ccttctcatg gtggctgtag aat
378 <210> SEQ ID NO: 16
380 <211> LENGTH: 24
382 <212> TYPE: DNA
384 <213> ORGANISM: Artificial Sequence
388 <220> FEATURE:
390 <223> OTHER INFORMATION: Primer
392 <400> SEQUENCE: 16
393 gtgtccttct catgggtggct gtag
396 <210> SEQ ID NO: 17
398 <211> LENGTH: 24
400 <212> TYPE: DNA
402 <213> ORGANISM: Artificial Sequence
406 <220> FEATURE:
408 <223> OTHER INFORMATION: Primer
410 <400> SEQUENCE: 17
411 gtgtccttct catgggtggct gtag
414 <210> SEQ ID NO: 18
416 <211> LENGTH: 23
418 <212> TYPE: DNA
420 <213> ORGANISM: Artificial Sequence
424 <220> FEATURE:
426 <223> OTHER INFORMATION: Primer
428 <400> SEQUENCE: 18
W--> 429 000
432 <210> SEQ ID NO: 19
434 <211> LENGTH: 23
436 <212> TYPE: DNA
438 <213> ORGANISM: Artificial Sequence
442 <220> FEATURE:
444 <223> OTHER INFORMATION: Primer
446 <220> FEATURE:
448 <221> NAME/KEY: misc_feature
450 <222> LOCATION: (18)..(18)
452 <223> OTHER INFORMATION: Fluorescently labeled

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Sum 8 → The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:49:59

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

```

456 <400> SEQUENCE: 19
457 ccttctcatg gtggctgtag aat
460 <210> SEQ ID NO: 20
462 <211> LENGTH: 24
464 <212> TYPE: DNA
466 <213> ORGANISM: Artificial Sequence
470 <220> FEATURE:
472 <223> OTHER INFORMATION: Primer
474 <220> FEATURE:
476 <221> NAME/KEY: misc_feature
478 <222> LOCATION: (22)..(22)
480 <223> OTHER INFORMATION: Fluorescently labeled
484 <400> SEQUENCE: 20
485 gtgtccttct catgggtggct gtag
488 <210> SEQ ID NO: 21
490 <211> LENGTH: 24
492 <212> TYPE: DNA
494 <213> ORGANISM: Artificial Sequence
498 <220> FEATURE:
500 <223> OTHER INFORMATION: Primer
502 <220> FEATURE:
504 <221> NAME/KEY: misc_feature
506 <222> LOCATION: (22)..(22)
508 <223> OTHER INFORMATION: Fluorescently labeled
512 <400> SEQUENCE: 21
513 gtgtccttct catgggtggct gtat
516 <210> SEQ ID NO: 22
518 <211> LENGTH: 25
520 <212> TYPE: DNA
522 <213> ORGANISM: Artificial Sequence
526 <220> FEATURE:
528 <223> OTHER INFORMATION: Primer
530 <220> FEATURE:
532 <221> NAME/KEY: misc_feature
534 <222> LOCATION: (23)..(23)
536 <223> OTHER INFORMATION: Labeled with fluoroscein
540 <400> SEQUENCE: 22
541 ctaccgggtg tctgtgtctc ggtag
544 <210> SEQ ID NO: 23
546 <211> LENGTH: 20
548 <212> TYPE: DNA
550 <213> ORGANISM: Artificial Sequence
554 <220> FEATURE:
556 <223> OTHER INFORMATION: Primer
558 <400> SEQUENCE: 23
559 cgtacctggc tatctgtgtc
562 <210> SEQ ID NO: 24
564 <211> LENGTH: 20
566 <212> TYPE: DNA

```

10/026,95

6

<210> 26

<211> 22

<212> DNA

<213> Artificial

see item 11 on Eno Summary Sheet

<400> 26

aacacacctg gctatctgtg tt

22

PSI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/026,952

DATE: 01/14/2002

TIME: 18:50:00

Input Set : A:\seqlist-0942 4980006 ascii

Output Set: N:\CRF3\01142002\J026952.raw

L:30 M:270 C: Current Application Number differs, Replaced Current Application No
 L:30 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:339 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
 L:429 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
 L:604 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
 L:608 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:608 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1015 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
 L:1033 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
 L:1051 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
 L:1469 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (71) SEQUENCE:
 L:1771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85
 L:1929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:92
 L:1947 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (93) SEQUENCE:
 L:2021 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (96) SEQUENCE:
 L:2299 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (107) SEQUENCE:
 L:2317 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (108) SEQUENCE:
 L:2443 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (115) SEQUENCE:
 L:2543 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (120) SEQUENCE:
 L:2561 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (121) SEQUENCE:
 L:2633 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (125) SEQUENCE:
 L:2715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129
 L:2771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131
 L:2881 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (136) SEQUENCE:
 L:2899 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (137) SEQUENCE:
 L:2917 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (138) SEQUENCE: